Reeves

PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/08/766,350A

164?

DATE: 07/14/98 TIME: 08:47:37

INPUT SET: S3230.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.



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SEQUENCE LISTING ENTERED
 1
 2
           General Information:
٠3
    (1)
 4
 5
          (i) APPLICANT: Chatterjee, Malaya
 6
                         Foon, Kenneth A.
 7
                         Chatterjee, Sunil K.
 8
         (ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
 9
10
                 11D10 AND METHODS OF USE THEREOF
11
12
        (iii) NUMBER OF SEQUENCES: 59
13
14
         (iv) CORRESPONDENCE ADDRESS:
15
               (A) ADDRESSEE: MORRISON & FOERSTER
               (B) STREET: 755 PAGE MILL ROAD
16
               (C) CITY: PALO ALTO
17
               (D) STATE: CA
18
19
               (E) COUNTRY: USA
               (F) ZIP: 94304-1018
20
21
          (v) COMPUTER READABLE FORM:
22
23
               (A) MEDIUM TYPE: Floppy disk
               (B) COMPUTER: IBM PC compatible
24
               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25
               (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27
         (vi) CURRENT APPLICATION DATA:
28
               (A) APPLICATION NUMBER: US 08/766,350
29
30
               (B) FILING DATE: 13-DEC-1996
31
               (C) CLASSIFICATION:
32
33
       (viii) ATTORNEY/AGENT INFORMATION:
               (A) NAME: Polizzi, Catherine M.
34
               (B) REGISTRATION NUMBER: 40,130
35
36
               (C) REFERENCE/DOCKET NUMBER: 30414-20003.21
37
38
         (ix) TELECOMMUNICATION INFORMATION:
39
               (A) TELEPHONE: (650) 813-5600
               (B) TELEFAX: (650) 494-0792
40
               (C) TELEX: 706141
41
42
43
     (2) INFORMATION FOR SEQ ID NO:1:
44
45
46
          (i) SEQUENCE CHARACTERISTICS:
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/766,350A

DATE: 07/14/98 TIME: 08:47:38

(A) LENGTH: 435 base pairs (B) TYPE: nucleic acid 49															IN	VPUT	SET:	S3230.raw
CO STRANDENNESS: single CO CO CO CO CO CO CO C										•	5							
Column C																		
S2										,								
53 54 55 56 61 (A) NAME/KEY: CDS 57 68 LOCATION: 1435 58 61 (A) NAME/KEY: mat_peptide 61 (B) LOCATION: 61 62 63 64 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 65 66 ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA 68 -20 -15 -10 -5 69 70 GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT 69 70 GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT 71 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser 72 1 5 10 73 74 GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC 75 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp 76 15 20 77 78 ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 79 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile 70 35 84 85 AGG CC GG ATC TAC GCC ACA TCC AGT TTA GGT TCT CGT GGT GCC CAAA 83 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys 84 85 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC 87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 88 89 80 AGC CTT GAG TG GAA GAT TTT GTA GCC TAT TAT CTT CTC ACC ATC AGC 288 87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 89 90 AGC CTT GAG TG GAA GAT TTT GTA GCC TAT TAT CTT CTC ACC ATC AGC 288 87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 89 90 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 91 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala 92 93 94 AGT TCT CCG TAC ACG TTC GGA GGG GAC AAG CTG GAA ATA AAA CGG 95 Ser Per Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 95 96 AGT TCT CCG TAC ACC TCC GGA GGG GAC AAG CTG GAA ATA AAA CGG 97 98 99 90 AGC CTT GAT GCA CCA ACT TC GGA GGG GAC AAG CTG GAA ATA AAA CGG 95 96 97 98 98 99 90 AGC CTG GAT GCA CCA ACC TCC GAT TCC CAC AGC CTG GAT ATC AGC 97 98 99 90 AGC CTG GAT GCA CCA ACT TCT GGA GGG GAC AAG CTG GAA ATA AAA CGG 98 99 90 AGC CTG GAT GCA CCA ACT TCT GGA GGG GAC AAG CTG GAA ATA AAA CGG 99 90 AGC CTG GAT GCA CCA ACT TCT GTA TCC ACC ACC ACC ACC TCC AGT AAG CTT 99 90 AGC CTG GAT GCT GCA																		
S4			(ii)	MO:	LECUI	LE T	YPE:	DNA	(gei	nomi	C)							
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ST			(ix)) FE	ATURI	Ξ:												
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Section				(1	B) L(OCAT:	ION:	14	135									
60 (A) NAME/KEY: mat_peptide 61 (B) LOCATION: 61 62 63 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 65 66 ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA 67 Met Gly Ala Pro Ala Gln I'le Leu Gly Phe Leu Leu Leu Leu Phe Pro 68 -20 -15 -10 -5 69 60 GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TTA TCT 96 71 Gly Thr Arg Cys Asp I'le Gln Met Thr Gln Ser Pro Ser Ser Leu Ser 72 1 5 10 73 74 GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC 75 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp 76 15 20 25 77 78 ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 79 I'le Gly I'le Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr I'le 80 30 35 40 81 82 AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 83 Lys Arg Leu I'le Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys 84 45 50 55 60 85 86 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 88 AGG TTC AGT GGA GAT AGA GAT TTT GTA GCC TAT TAC TGT CTC ACC ATC AGC 88 ATG Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 89 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 89 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 89 AGT TCT CCG TAC ACG TTC GGA GGG ACC AAG CTG GAA ATA AAA CGG 90 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 91 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 92 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 93 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 96 97 GCT GAT GCT GCA CCA ACT GTA TCC ATC TCC CCA CCA TCC AGT AAG CTT 97 A12 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TCC CCA CCA TCC AGT AAG CTT 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TCC CCA CCA TCC AGT AAG CTT			(ix)) FE	ATURI	3:												
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64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 656 667 ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA 668 -20																		
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68		_																48
69 70			Gly	Ala	Pro	Ala		Ile	Leu	GLY	Phe		Leu	Leu	Leu	Phe		
70		-20					-13					-10					-5	
72		GGT	ACC	AGA	TGT	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	TTA	TCT	96
73 74 GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC 75 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp 76 15 20 25 77 78 ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 79 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile 80 30 35 40 81 82 AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 83 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys 84 45 50 55 60 85 86 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 288 87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 88 65 70 75 89 90 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 336 91 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala 92 80 85 90 94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 96 97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432		Gly	Thr	Arg	Cys	_	Ile	Gln	Met		Gln	Ser	Pro	Ser		Leu	Ser	
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77 78 ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 79 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile 80 30 35 40 81 82 AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 83 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys 84 45 50 55 60 85 86 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 88 65 70 75 89 90 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 91 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala 92 80 85 90 93 94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 96 95 100 105 97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432																		
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80																		1,72
82 AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 240 83 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys 60 84 45 50 55 60 86 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 288 87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 70 75 89 65 70 75 75 89 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 336 336 91 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala 85 90 93 85 90 93 85 90 94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 95 96 95 100 97 105 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA CCA AGT AAG CTT	80		-					_						_	_			
83 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys			~~~	ama	3 m.c		999	202	maa	3 C/III	mm »	aam	mam	aam	ama	000	777	240
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86 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 288 87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 70 75 88 65 70 75 89 90 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 336 91 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala 90 92 80 85 90 93 93 94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 96 95 100 105 97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432		-	*****	БСи	***	-1-			501	501	Lea	-		1			-	
87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser 88 65 70 75 89 90 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 91 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala 92 80 85 90 93 94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 96 95 100 105 97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432																		
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89 90 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 91 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala 92 80 85 90 93 94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 96 95 100 105 97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432		Arg	Pne	Ser	GIY		Arg	ser	GIY	ser	_	TYL	ser	ьец	lnr		ser	
91 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala 92 80 85 90 93 94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 96 95 100 105 97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432											. •							
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93 94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 96 95 100 105 97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432		Ser	Leu	Glu		Glu	Asp	Phe	Val		Tyr	Tyr	Cys	Leu		Tyr	Ala	
94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384 95 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg 96 95 100 105 97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432					80					85					90			
96 95 100 105 97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432		AGT	TCT	CCG	TAC	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAA	ATA	AAA	CGG	384
97 98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432		Ser	Ser		Tyr	Thr	Phe	Gly		Gly	Thr	Lys	Leu		Ile	Lys	Arg	
98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432				95					100					105				
		GCT	GAT	GCT	GCA	CCA	ACT	GTA	TCC	ATC	TTC	CCA	CCA	TCC	AGT	AAG	CTT	432
JJ Ald Asp Ald Ald 110 111 val bot 110 110 110 bot bot by bod	99																	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/766,350A

DATE: 07/14/98 TIME: 08:47:40

INPUT SET: S3230.raw GGG Gly (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ile Asn Leu His Trp Leu Gln Glu Pro Asp Gly Thr Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu Gly (2) INFORMATION FOR SEQ ID NO:3:

150 (i) SEQUENCE CHARACTERISTICS: 151 (A) LENGTH: 461 base pairs

151 (A) LENGTH: 401 base pa 152 (B) TYPE: nucleic acid

RAW SEQUENCE LISTING PATENT APPLICATION US/08/766,350A

DATE: 07/14/98 TIME: 08:47:43

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154			(1) T(OPOLO	OGY:	line	ear									
155																	
156		(ii)	MOI	LECUI	LE T	YPE:	DNA	(ger	nomi	2)							
157		` '						-									
158																	
159		/iv)	FEA	ופוזיי	F.												
		(11)				KEY:	CDC										
160					-			450									
161			1)	3) L(JCAI.	ION:	1	103									
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164						KEY:	_	_pept	ide								
165			(E	3) L(CAT:	ION:	58										
166																	
167																	
168		(xi)	SEC	QUEN	CE DI	ESCRI	[PTIC	N: S	SEQ :	ED NO	0:3:						
169																	
170	ATG	GAA	TGC	AGC	TGG	GTC	TTT	CTC	TTC	CTC	CTG	TCA	ATA	ACT	ACA	GGT	48
171						Val											
172	-19		-1-		-15	-				-10					-5	-	
173																	
174	GTC	CAC	TCC	CAG	CCT	TAT	СТА	CAG	CAG	тст	GGG	GCT	GAG	CTG	GTG	AGG	96
175						Tyr											
176	vai	птъ	261	1	ALG	- Y -	пси	5	0111	UCI	Cry	7124	10	шси	val	****9	
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177			000	ma.	ama.		3 m.a	maa	maa	770	COM	mam	aaa	ma a	7 (7	TOTAL CO	111
178						AAG											144
179	Ser	-	Ala	Ser	Val	Lys		Ser	Cys	гĀг	Ата		GIY	Tyr	Thr	ьeu	
180		15					20					25					
181																	
182						CAC											192
183	Thr	Ser	Tyr	Asn	Met	His	\mathtt{Trp}	Val	Lys	Gln	Thr	Pro	Gly	Gln	Gly	Leu	
184	30					35					40					45	
185																	
186	GAA	TGG	ATT	GGA	AAT	ATT	TTT	CCT	GGA	AAT	GGT	GAT	ACT	TAC	TAC	AAT	240
187	Glu	Trp	Ile	Gly	Asn	Ile	Phe	Pro	Gly	Asn	Gly	Asp	Thr	Tyr	Tyr	Asn	
188		•		-	50				_	55	_	_		_	60		
189																	
190	CAG	AAG	TTT	AAG	GGC	AAG	GCC	TCA	TTG	ACT	GCA	GAC	ACA	TCC	TCC	AGC	288
191						Lys											
192	0211	_,_		65	U -1	-1-			70					75			
193				0,5					, 0								
194	አሮአ	ccc	TAC	λπα	CAG	ATC	ACC	AGC	СТС	ACA	тст	CAA	GAC	ጥርጥ	GCG	GTC	336
195						Ile											330
	IIII	мта	_	MEC	GIII	116	SCI	85	пец	1111	Der	Giu	90	JCI	AIU	٧٨١	
196			80					65					90				
197			m~~	~~-	707	~~~	77~	шаа	0 x 0	aam.	COTT	ama	ana	TIN C	שממ	C) C) T)	204
198						GGG											384
199	Tyr		Cys	Ala	Arg	Gly		Trp	GLu	GTA	ата		Asp	туr	Trp	GTÀ	
200		95					100					105					
201																	
202						ACC											432
203	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ala	Lys	Thr	Thr	Pro	Pro		
204	110					115					120					125	
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207	Val	Tyr	Pro	Leu		Pro	Gly	Ser	Leu									
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234	Glu	${\tt Trp}$	Ile	Gly	Asn	Ile	Phe	Pro	Gly	Asn	Gly	Asp	Thr	Tyr	Tyr	Asn		
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